AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

On page 5, please amend the paragraph beginning on line 10 to recite as follows:

~~FIG. 3~~ FIGS. 3A-3C. Nucleotide and deduced amino acid sequences of the human sperm protein FSP95. The deduced amino acid sequence (SEQ ID NO:2) of human sperm FSP95 is shown below the cDNA sequence (SEQ ID NO:1). The numbers on the left refer to the nucleotide sequence; numbers on the right refer to the amino acid sequence. The consensus ATG of the open reading frame and the polyadenylation signal ~~(ATTFAAA)~~ ATTAAA are indicated in bold letters. The termination codon (TAA) is marked with an asterisk. The 5-prime and 3-prime untranslated regions are 162 bp and 218 bp, respectively, and are shown in italics. The calculated molecular weight and ~~pI~~ pI of the predicted protein were 94.6 kDa and 6.0, respectively. The 18 underlined sequences indicate the tryptic peptides obtained by microsequencing. The putative tyrosine kinase phosphorylation site is indicated in bold within a box (residue number 435). The nucleic acid sequence was submitted to the GenBank (accession number AF087003).

On page 5, please amend the paragraph beginning on line 21 to recite as follows:

~~FIG. 4~~ FIGS. 4A-4B. Homology comparison of the deduced amino acid sequences of human sperm FSP95 with those of mouse (SEQ ID NO:3) and human (SEQ ID NO:4) sperm fibrous sheath AKAPs (mouse: pro-mAKAP82, accession # ~~148968~~ AAC83697; human: pro-hAKAP82, accession # AF072756). The sequences were listed in descending order of homology from the FSP95. The alignment was constructed by use of the GCG-PILEUP program and formatted with ALSCRIPT version 2.0. The shaded areas indicate the amino acid identities and similarities among the molecules (cut off 8 in ALSCRIPT). The conserved AKAP-like intracellular targeting domains are shown in boxes. The N-terminal RII-binding domain of the mouse and human AKAP82 is highlighted with an underline.

On page 8, please amend the paragraph beginning on line 32 to recite as follows:

The invention provides the nucleotide sequences of *FSP95* nucleic acids which were identified by screening a human testicular cDNA library screened with a degenerate primers designed from a peptide sequence obtained from purified FSP95. Nucleic acid sequences of the identified *FSP95* genes are described herein. As used herein, "a *FSP95* nucleic acid" refers to:

(a) a nucleic acid molecule containing the nucleotide sequence of *FSP95* shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1);

(b) any nucleotide sequence that encodes a polypeptide containing the amino acid sequence of FSP95 shown in ~~FIG. 3 and FIG. 4~~ FIGS. 3A-3C and FIGS. 4A-4B (SEQ ID NOS:2, 3, 4);

(c) any nucleotide sequence that hybridizes to the complement of the DNA sequences that encode any of the amino acid sequences of FSP95 shown in ~~FIG. 3 and FIG. 4~~ FIGS. 3A-3C and FIGS. 4A-4B (SEQ ID NOS:2, 3, 4) under highly stringent conditions, *e.g.*, hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel F.M. *et al.*, eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at p. 2.10.3); and/or

(d) any DNA sequence that hybridizes to the complement of the DNA sequences that encode any of the amino acid sequences in FSP95 shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1), under less stringent conditions, such as moderately stringent conditions, *e.g.*, washing in 0.2xSSC/0.1% SDS at 42°C (Ausubel *et al.*, 1989, *supra*), and encodes a gene product functionally equivalent to a *FSP95* gene product.

On page 11, please amend the paragraph beginning on line 8 to recite as follows:

As used herein, a *FSP95* PKA RII subunit binding domain sequence includes:

(a) any DNA sequence that encodes a peptide, *e.g.*, a PKA RII subunit binding domain peptide, comprising amino acids 318-335 (LKKVLLKHAKEVVSDLID) (SEQ ID NO:5), 368-385 (QKATDIMDAMLRKLYNVM) (SEQ ID NO:6), or 671-688 (EHLMNSVMKLCVIIAKSC) (SEQ ID NO:7);

(~~B~~ b) any DNA sequence that hybridizes to the complement of the DNA sequences that encode the PKA RII subunit binding domain sequences described in (a) ~~or (b)~~ under highly stringent conditions, *e.g.*, hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel F.M. *et al.*, eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & Sons, Inc., New York, at p. 2.10.3); and/or

(c) any DNA sequence that hybridizes to the complement of the DNA sequences that encode the PKA RII subunit binding domain sequences described in (a) or (b) under less stringent conditions, such as moderately stringent conditions, *e.g.*, washing in 0.2xSSC/0.1% SDS at 42°C (Ausubel *et al.*, 1989, *supra*), and encodes a gene product functionally equivalent to a *FSP95* PKA RII subunit binding domain.

On page 11, please amend the paragraph beginning on line 33 to recite as follows:

FSP95 sequences of the present invention are derived from a eukaryotic genome, preferably a mammalian genome, and more preferably a human genome. In a specific embodiment, the nucleotides of the present invention encompass any DNA sequence derived from a mammalian genome which hybridizes under highly stringent conditions to the nucleotide sequence shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1). In a specific embodiment, the nucleotides of the present invention encompass any DNA sequence derived from a mammalian genome which hybridize under highly stringent conditions to the nucleotide sequence shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1) and encodes a gene product involved sperm motility, and contains a PKA RII subunit binding domain.

On page 12, please amend the paragraph beginning on line 10 to recite as follows:

The invention further includes regulator nucleic acids of the *FSP95* gene. The genomic sequence of the *FSP95* gene contains regulatory sequences in the non-coding 5'-flanking region. The 5'-regulatory sequences of the *FSP95* gene comprise the polynucleotide sequences located between the nucleotide in position -5000, -3000, -2000, -1000, or -500, and the nucleotide in position +10, +100, or +300, of the nucleotide sequence of the nucleotide sequence shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1).

On page 12, please amend the paragraph beginning on line 35 to recite as follows:

In yet another embodiment, the *FSP95* nucleic acid sequences of the invention are nucleic acid sequences encoding FSP95 gene products containing polypeptide portions corresponding to (that is, polypeptide portions exhibiting amino acid sequence similarity to) the amino acid sequences depicted in ~~FIG. 3 and FIG. 4~~ FIGS 3A-3C and FIGS. 4A-4B (SEQ ID NOS:2, 3, 4), wherein the corresponding portion exhibits greater than about 50% amino acid identity with the depicted sequence, averaged across the FSP95 gene product's entire length.

On page 13, please amend the paragraph beginning on line 5 to recite as follows:

In specific embodiments, FSP95 encoding nucleic acids comprise the cDNA sequences of the nucleotide sequences shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1) or the coding regions thereof, or nucleic acids encoding a FSP95 protein (*e.g.*, a protein having the amino acid sequences depicted in ~~FIG. 3 and FIG. 4~~ FIGS. 3A-3C and FIGS. 4A-4B (SEQ ID NOS:2, 3, 4). The invention provides isolated or purified nucleic acids consisting of at least 8 nucleotides (*i.e.*, a hybridizable portion) of a *FSP95* nucleic acid sequence; in other

embodiments, the nucleic acids consist of at least 25 (continuous) nucleotides, 50, 100, 150, 200, 300, 400, 500, 600, 700, 800,900, 1000, 1500, 2000, 2500, 2900, or 2941 contiguous nucleotides of a *FSP95* sequence, or a full-length *FSP95* coding sequence. For example, in one embodiment the invention provides isolated or purified nucleic acids consisting of nucleotides 1-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-750, 751-1000, 1001-1501, or 1501-2000, 2001-2500, or 2501-2941, of the nucleotide sequence shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1). In another embodiment, the nucleic acids are smaller than 25, 50, 75, 100, 200, 300, 400, 500, 1000, 1500, 2000, 2500, or 2941 nucleotides in length. Nucleic acids can be single or double stranded. The invention also provides nucleic acids hybridizable to or complementary to the foregoing sequences. In specific aspects, nucleic acids are provided which comprise a sequence complementary to at least 10, 25, 50, 100, 200, 300, 400, 500, 1000, 1500, 2000, 2500 nucleotides or the entire coding region of a *FSP95* gene. As will be understood by those skilled in the art, the invention also encompasses those genomic DNA sequences which give rise to the cDNA sequences of the nucleotide sequences shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1) described above.

On page 13, please amend the paragraph beginning on line 25 to recite as follows:

In addition to the human *FSP95* nucleic acid sequences disclosed in the nucleotide sequences shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1), other *FSP95* nucleic acid sequences can be identified and readily isolated, without undue experimentation, by molecular biological techniques well known in the art, used in conjunction with the *FSP95* nucleic acid sequences disclosed herein. These other sequences are encompassed by the present invention. For example, additional human *FSP95* nucleic acid sequences at the same or at different genetic loci as those disclosed in the nucleotide sequences shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1) can be isolated readily. There can exist, for example, genes at other genetic or physical loci within the human genome that encode proteins that have extensive homology to one or more domains of the *FSP95* gene products and that encode gene products functionally equivalent to a *FSP95* gene product. Further, homologous *FSP95* nucleic acid sequences present in other species can be identified and isolated readily.

On page 14, please amend the paragraph beginning on line 1 to recite as follows:

With respect to identification and isolation of *FSP95* nucleic acid sequences present at the same genetic or physical locus as those sequences disclosed in the nucleotide sequences shown in ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1), such sequences can, for example, be obtained readily by utilizing standard sequencing and bacterial artificial chromosome (BAC) and P1 artificial chromosome (PAC) technologies.

On page 17, please amend the paragraph beginning on line 14 to recite as follows:

The amino acid sequences depicted in ~~FIG. 3 and FIG.4~~ FIGS. 3A-3C and FIGS. 4A-4B (SEQ ID NOS:2, 3, 4) represent *FSP95* gene products. The *FSP95* gene product, sometimes referred to herein as a "FSP95", includes those products encoded by the *FSP95* nucleic acid sequences described in Section 5.1, above. In accordance with the present invention, the nucleic acid sequences encoding the *FSP95* gene products are derived from eukaryotic genomes, including mammalian genomes. In a preferred embodiment the nucleic acid sequences encoding the *FSP95* products are derived from the human genome.

On page 27, please amend the paragraph beginning on line 12 to recite as follows:

Various procedures known in the art may be used for the production of polyclonal antibodies to a FSP95 or derivative or analog. In a particular embodiment, rabbit polyclonal antibodies to an epitope of an FSP95 encoded by a sequence as shown in ~~FIG.3~~ FIGS. 3A-3C (SEQ ID NO:1) or a subsequence thereof, can be obtained. For the production of antibody, various host animals can be immunized by injection with the native FSP95, or a synthetic version, or derivative (*e.g.*, fragment) thereof, including but not limited to rabbits, mice, rats, etc. Various adjuvants may be used to increase the immunological response, depending on the host species, and including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. For preparation of monoclonal antibodies directed toward an FSP95 sequence or analog thereof, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, Nature 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, Immunology Today 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals (see PCT International Publication No. WO 89/12690, published December 12, 1989). According to the invention, human antibodies may be used and can be obtained by using human hybridomas (Cote et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:2026-2030) or by transforming human B cells with EBV virus *in vitro* (Cole et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, pp. 77-96). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, Proc. Natl. Acad. Sci. U.S.A. 81:6851-6855; Neuberger et al., 1984, Nature 312:604-608;

Takeda et al., 1985, Nature 314:452-454) by splicing the genes from a mouse antibody molecule specific for FSP95 together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention.

On page 32, please amend the paragraph beginning on line 1 to recite as follows:

The genomic sequence of the *FSP95* gene contains regulatory sequences both in the non-coding 5'-flanking gene of polynucleotide sequence of ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1) can be assessed by any known method. In one embodiment, methods for *FSP95* gene comprise the polynucleotide sequences located between the nucleotide in position -2000 and the nucleotide in position +100 of the nucleotide sequence of ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1) or more preferably between positions -3000 and +200 of ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1).

On page 32, please amend the paragraph beginning on line 7 to recite as follows:

Methods for identifying the 5'-regulatory sequences of the *FSP95* polynucleotide fragments of ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1) involved in the regulation of the expression of the *FSP95* gene are well-known to those skilled in the art (see Sambrook et al., Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989). An example of a typical method that can be used involves a recombinant vector carrying a reporter gene and genomic sequences from the *FSP95* genomic promoter sequence of ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1). Briefly, the expression of the reporter gene (for example, green fluorescent protein, luciferase, β-galactosidase, or chloramphenicol acetyl transferase) is detected when placed under the control of a biologically active polynucleotide fragment. Genomic sequences located upstream of the first exon of the gene may be cloned into any suitable promoter reporter vector, such as the pSEAPBasic, pSEAP-Enhancer, pβgal-Basic, pβgal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech, or pGL2-basic or pGL3-basic promoterless luciferase reporter gene vector from Promega. Each of these promoter reporter vectors include multiple cloning sites positioned upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, green fluorescent protein, luciferase, or β-galactosidase. The sequences upstream of the first *FSP95* exon are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The level of reporter protein is assayed and compared to the level obtained with a vector lacking an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert.

On page 33, please amend the paragraph beginning on line 16 to recite as follows:

Thus, the present invention also provides a purified, isolated, and recombinant nucleic acid comprising a polynucleotide sequence located between the nucleotide in position -2000 and the nucleotide in position +100 of the nucleotide sequence of ~~FIG. 3~~ FIGS 3A-3C (SEQ ID NO:1), or a sequence complementary thereto or a functionally active fragment thereof.

On page 33, please amend the paragraph beginning on line 20 to recite as follows:

By a "functionally active" fragment of the sequence of ~~FIG. 3~~ FIGS. 3A-3C (SEQ ID NO:1) according to the present invention is intended a polynucleotide comprising or alternatively consisting of a fragment of said polynucleotide which is functional as a regulatory region for expressing a recombinant polypeptide or a recombinant polynucleotide in a recombinant cell host. For the purpose of the invention, a nucleic acid or polynucleotide is "functional" as a regulatory region for expressing a recombinant polypeptide or a recombinant polynucleotide.

On page 34, please amend the paragraph beginning on line 22 to recite as follows:

As described in more detail in Section 6 below, motif analysis identified three PKA RII subunit binding domains at amino acids 318-335 (LKKVLLKHAKEVVSDLID) (SEQ ID NO:5), 368-385 (QKATDIMDAMLRKLYNVM) (SEQ ID NO:6), and 671-688 (EHLMNSVMKLCVIIAKSC) (SEQ ID NO:7) of ~~FIG.3~~ FIGS. 3A-3C.

On page 35, please amend the paragraph beginning on page 6 to recite as follows:

In one embodiment, the invention also encompasses the use of FSP95 promoter sequences either alone, respectively, in which the FSP95 promoter sequences can be used to drive spermatid-specific expression of drugs or toxins using gene therapy techniques in cells of a patient with a testes-specific proliferative disorder or cancer to inhibit growth or kill the cancer cell. In another embodiment, gene therapy techniques using promoter constructs either alone, or in combination with the nucleic acid sequences encoding the PKA RII subunit binding domain set forth in amino acids 318-335 (LKKVLLKHAKEVVSDLID) (SEQ ID NO:5), 368-385 (QKATDIMDAMLRKLYNVM) (SEQ ID NO:6), and 671-688 (EHLMNSVMKLCVIIAKSC) (SEQ ID NO:7) of ~~FIG. 3~~ FIGS. 3A-3C, respectively, can be used to drive spermatid-specific expression of drugs or toxins can be used for sterilization or contraception in the testis.

On page 42, please amend the paragraph beginning on line 2 to recite as follows:

A completely degenerate deoxyinosine containing sense primer (5'-A/T-C/G-I GTI TT-C/T TT-C/T AA-C/T TT-C/T A/T/C-TI A/C-GI-3') (SEQ ID NO:8) was designed from one of the microsequences obtained by mass spectrometry, peptide number 6 (SVFFNFI/LR) (SEQ ID NO:9), and the oligonucleotide was synthesized by GIBCO BRL (Life Technologies, CA). Using this forward primer and an adapter primer, a 3' rapid amplification of cDNA ends (RACE) polymerase chain reaction (PCR) was performed using 0.25 ng of human testicular Marathon ready cDNA (Clontech, CA) in a 25 μl assay system for 40 cycles. Thermal cycling was done in a MJ Research (Watertown, MA) thermal cycler (PTC-200 DNA engine) using a program of one cycle at 94°C for 1.5 min and 40 cycles of 94°C for 30 sec, 46°C for 1 min and 68°C for 2 min. PCR products were separated on a 1.7% NuSieve (FMC, ME) agarose gel. A 1.0 kb DNA fragment was isolated, reamplified, cloned into -the pCR 2.1 -TOPO vector (Invitrogen, CA), and sequenced on a Perkin-Elmer Applied Biosystems DNA sequencer using big fluorescence dye terminator chemistry with Tao DNA polymerase. The 3' clone contained a 786 bp open reading frame and a 218 bp untranslated region. The 5' end of the cDNA was also amplified by 5' RACE PCR from the same template using an adapter primer and an antisense 3' gene specific primer (5'-AGC CTG GGG GGA GAA ~~GAG~~ GAC GCC AAC ~~GOT~~ GGT C-3') (SEQ ID NO:10) which was 118 bp downstream from the 5' end of the 1.0 kb 3' clone. A product of 2081 bp was obtained and cloned into the pCR 2.1-TOPO vector. The 5' clone revealed a 162 bp untranslated region and an open reading frame of 1919 bp. cDNA clones were sequenced in both directions using vector-derived and insert specific primers. The nucleotide and amino acid sequence data were analyzed using the Genetics Computer Group program package (*Wisconsin Package Program Manual,* Version 9, Madison, WI).

On page 47, please amend the paragraph beginning on line 2 to recite as follows:

To obtain structural information on the identity of one of the 95 kDa tyrosine phosphorylated antigens, microsequencing of a Coomassie stained 2-D SDS-PAGE protein spot was undertaken. The location of the spot cored from the 2-D gel is indicated by a white circle in Fig. 1A. Because of the low amount of the protein available in a well resolved 2-D gel, amino acid sequencing was performed by tandem mass spectrometry on peptides generated by overnight trypsin digestion at 37°C of the protein spot within pieces of the gel. The extracted peptides were concentrated and analyzed by capillary column liquid chromatography electrospray- tandem mass spectrometry. A total of 18 peptide sequences were obtained ~~(Table 1)~~. Database searches using both the molecular weight information (mass mapping by MS-Fit) and sequence information by using Fasta (Pearson and Lipman,

1988, Proc. Natl. Acad. Sci. USA 85:2444-2448), allowing a 15% gel derived protein mass tolerance and a 1 Da peptide mass tolerance, did not identify any known protein.

On page 47, please amend the paragraph beginning on line 17 to recite as follows:

To isolate the cDNA encoding the 95 kDa tyrosine phosphorylated protein, a completely degenerate inosine containing forward primer designed from peptide number 6 ~~(Table 1)~~ was used to amplify a 1.0 kb piece of cDNA by 3' RACE PCR from human testicular Marathon ready cDNA (Clontech, CA). The 5' cDNA including an untranslated region was also cloned by PCR producing a 2.1 kb cDNA with a 118 bp overlap at the 3' end. The nucleotide sequence of the full-length cDNA ~~(Fig. 3)~~ (Figs. 3A-3C) consists of 2942 bp with an in-frame start codon at nucleotides 163-165 conforming to a Kozak consensus for the translation initiation site (Kozak, 1991, J. Biol. Chem. 266:19867-19870). The translation start site was further authenticated by the presence of two in frame stop codons at 45 bp and 72 bp upstream of the first ATG sequence. The cDNA contained a 2559 bp open reading frame with untranslated regions of 162 bp at the 5' end, 218 bp at the 3' end, and a polyadenylation signal (ATTAAA) (Juretic and Theus, 1991, FEBS Lett. 290:4-8) 11 bp upstream from the poly(A) tail. The open reading frame encodes a protein of 853 amino acids with a predicted molecular weight of 94.6 kDa and a pI of 6.0. All of the 18 tryptic peptides obtained by microsequencing the 95 kDa protein spot were recovered in the predicted amino acid sequence of the molecule ~~(Fig. 3), underlines)~~ (Figs. 3A-3C, underlines), validating that the protein originally identified and cored from the gel had been cloned.

On page 48, please amend the paragraph beginning on line 10 to recite as follows:

Comparison of the deduced FSP95 sequence to the GenBank data base using BLAST (Altschul et al., 1990, J. Mol. Biol. 215:403-410) and FASTA (Pearson and Lipman, 1988, Proc. Natl. Acad. Sci. USA 85:2444-2448) revealed that the human sperm FSP95 had closest amino acid identity to a mouse sperm fibrous sheath AKAP, precursor of mouse AKAP82 (pro-mAKAP82) (identity: 33.6%; similarity: 42.5%), and to a human sperm fibrous sheath AKAP, precursor of human AKAP82 (pro-hAKAP82) (identity: 32.4%; similarity: 39.4%) (Turner et al., 1998, J. Biol. Chem. 273:32135-32141, Carrera et al., 1994, Dev. Biol. 165:272-284). The amino acid sequence alignment of these proteins revealed that the middle and part of the N-terminal and C-terminal regions of these molecules contained conserved domains ~~(Fig. 4)~~ (Figs. 4A-4B). The overall identities between FSP95 and these AKAPs suggest that the human sperm FSP95 is encoded by a previously unreported gene. Interestingly, the two potential intracellular anchoring domains of mouse sperm pro-mAKAP82 (Carrera et al., 1994, Dev. Biol. 165:272-284) were conserved in both the pro-

hAKAP82 (Turner et al., 1998, J. Biol. Chem. 273:32135-32141) and the human sperm FSP95 cDNAs. Both these intracellular targeting regions were located in the highly basic N-terminal region while the C-termini of these proteins were more acidic, containing residues with long aliphatic side chains. However, the RU-binding domains of human and mouse AKAP82 were not conserved in FSP95.

On page 50, please amend the paragraph beginning on line 18 to recite as follows:

In this report we describe the cloning and characterization of a novel human sperm antigen, designated FSP95 in consideration of its fibrous sheath localization and calculated molecular weight of 95 kDa. In order to characterize FSP95 from a 2-D SDS-PAGE protein spot derived microsequence, the 3' cDNA of the molecule was amplified using a single gene-specific inosine containing primer and an adapter primer from human testicular Marathon cDNA. The obtained cDNA revealed the presence of 4 FSP95 microsequenced peptides embedded in its open reading frame. The 5' end of the cDNA was then similarly cloned by 5' RACE revealing two in frame stop codons upstream of the most 5' methionine identified. This indicates that the reported cDNA represents the complete coding sequence of FSP95. The translation start site also conforms to the essential Kozak consensus sequence. Embedded within the deduced amino acid sequence are all 18 microsequenced peptides obtained from the FSP95 protein spot ~~(Table 1; Fig. 3)~~ (Figs. 3A-3C) validating that the protein spot originally cored was cloned. The success of this cloning strategy using a single microsequence derived primer is important because it was completed in only about three weeks. Therefore, this approach may be an important avenue in converting microsequence data into complete sequence information and highlights the increasing importance of proteome based cloning.

On page 50, please amend the paragraph beginning on line 35 to recite as follows:

From a methodological view it is important to note that the peptide sequence used to initiate the cloning experiment (peptide 6 ~~, Table 1~~) was confirmed by combining interpretation of the CAD spectrum of the peptide in the digest, interpretation of the CAD spectrum of the N-terminal derivatized peptide (Cardenas et al., 1997, Rapid Commun. Mass Spectrom. 11:1271-1278) and comparison of CAD spectra of the digest peptide with a synthetic peptide. Minor discrepancies were observed in comparing the amino acid sequences derived from the mass spectrometry data and the cDNA data for peptides 6, 12 and 18 due to changes in a single base. The differences produce an F to S substitution in peptide 6, either an E to V or a T to A substitution in peptide 12 and an E to G substitution in peptide 18. These substitutions could be due to an inter-individual DNA polymorphism between the

donors from which FSP95 was microsequenced and the donor from whom the Clontech Marathon testicular cDNA was constructed.

On page 52, please amend the paragraph beginning on line 8 to recite as follows:

Comparison of the deduced amino acid sequence of the FSP95 cDNA with the available database reveals its highest homology with mouse and human sperm pro-AKAP82 (34% and 32% amino acid identity, respectively), which are protein kinase A anchor proteins that sequester PK-A to subcellular locations. This suggests that FSP95 with these AKAPs reveals that FSP95 possesses two potential intracellular targeting domains ~~(Fig. 4)~~ (Figs. 4A-4B). Both these domains lie within an N-terminal basic region similar to the AKAPs 75 and 79 (Glantz et al., 1993, J. Biol. Chem. 268:12796-12804, Carr et al., 1992, J. Biol. Chem. 267:6816-16823). Interestingly, however, the predicted RII-binding domain of these sperm AKAPs was found to be lacking in FSP95 as judged by poor conservation and lack of the putative amphipathic helix binding motif in this region (Carr et al., 1991, J. Biol. Chem. 266:14188-14192). In a recent study, the presence of an AKAP of approximately 110 kDa and the regulatory subunits of PK-A (RIIα, RIIβ and RIβ) has been demonstrated in human, bovine and monkey spermatozoa (Vijayaraghavan et al., 1997, J. Biol. Chem. 272:4747-4752). Moreover, it has been suggested that the anchoring of the regulatory subunity of PK-A to bovine sperm AKAP, independent of PK-A catalytic activity, is essential for the regulation of sperm motility (Vijayaraghavan et al., 1997, J. Biol. Chem. 272:4747-4752). Therefore, considering the unique testis specific expression pattern of FSP95 (Fig. 5), and its similarity to sperm AKAPs FSP95 could be explored for the possible development of a cell permeable anchoring inhibitor peptide for the formulation of a topical spermiostatic agent for human. Furthermore, the identification of FSP95 as a tyrosine kinase substrate and its similarity to sperm AKAP may suggest possible interrelationship between PK-A and tyrosine kinase signaling pathways, because tyrosine phosphorylation and capacitation in other mammals has been shown to be upregulated by a cAMP/PK-A dependent pathway (Visconti and Kopf, 1998, Biol. Reprod. 59:1-6, Galantino-Homer et al., 1997, Biol. Reprod. 56:707-719, Visconti et al., 1995, Development 121:1139-1150).